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1600

RAW SEQUENCE LISTING

DATE: 12/06/2003

PATENT APPLICATION: US/09/830,111E

TIME: 10:42:19

Input Set : A:\21581-265.seq.V3.ST25.txt

Output Set: N:\CRF4\12062003\I830111E.raw

3 <110> APPLICANT: Kaneka Corporation
 4 Matsuda, Hideyuki
 5 Kawamukai, Makota
 6 Yajima, Kazuyoshi
 7 Ikenaka, Yasuhiro
 8 Hasegawa, Junzo
 9 Takahashi, Satomi
 11 <120> TITLE OF INVENTION: Process For Producing Coenzyme Q10
 13 <130> FILE REFERENCE: 21581-00265-US
 15 <140> CURRENT APPLICATION NUMBER: 09/830,111E
 16 <141> CURRENT FILING DATE: 2001-07-23
 18 <160> NUMBER OF SEQ ID NOS: 9
 20 <170> SOFTWARE: PatentIn version 3.2
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 1653
 24 <212> TYPE: DNA
 25 <213> ORGANISM: Saioella complicata
 27 <400> SEQUENCE: 1

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30	gagattgagt	tcaggacaaa	gctttgatcc	gtgaggtcta	catcttcagc	aaatcatttc	120
32	aaatccatat	accatggcct	caccagcact	gcggatacga	agcatcagct	ctcgatcaat	180
34	cgccctctctg	cgatcggtta	ccctaagaac	agcctcggca	ccttcattac	gactaagatg	240
36	taccccgacg	agccggccat	cgagttcatg	ggctgctgct	gtgtcttcgg	cgtcgagact	300
38	ggttgagcct	gatccgaatc	aacctctcat	caatccgctc	aacttggtcg	gtcccagatg	360
40	gtcaaattctt	acatccaaca	tccgatctct	cctcggttca	ggacaccctt	ctctcgacac	420
42	tgctcgctaaa	tactatgttc	agtctgaggg	aaagcatatt	cgtccgctca	tggtactgct	480
44	gatggctcag	gcgacggagg	ttgcgcaaaa	agttcagggg	tgggagaagg	tcgtggagggt	540
46	tccggtgaac	gagggactcg	caccaccaga	ggtgctcaat	gacaagaacc	cagatatgat	600
48	gaacatgagg	tcaggaccat	taacgaagga	cggcgagatc	gagggacaga	cgtcgaatat	660
50	cctcgccctcg	caacggcggt	tggctgagat	cacggagatg	atccatgcag	catcactcct	720
52	ccacgacgac	gttatcgacg	cttccgagac	cagacgaaac	gcaccatccg	gaaaccaggc	780
54	attcggaaac	aagatggcga	ttttggctgg	tgatttcttg	ttgggacggg	cgtctgttgc	840
56	attggcgagg	ttgcgcaatc	cggaggtgat	tgagcttttg	gctactgtta	ttgcaaactt	900
58	ggttgagggg	gagttcatgc	agttgaaaaa	tactgttgat	gatgcgattg	aggctacggc	960
60	gacgcaggaa	acgttcgatt	actatttgca	gaagacttac	ttgaagactg	cgtccttgat	1020
62	tgccaagtgc	tgacagagca	gtgcgcttct	gggtgggtgct	acgcctgagg	ttgctgatgc	1080
64	tgcttatgct	tacggaagga	accttggttt	ggcattccag	atcgctcgacg	acatgctcga	1140
66	ctacaccgtc	tccgctaccg	acctcggtaa	gcccgcgggt	gcagacctcc	agctcggtct	1200
68	cgccaccgcg	ccggccctct	tcgcatggaa	gcaccacgcc	gagctcggtc	ccatgatcaa	1260
70	gcgcaagttc	tctgacccag	gagacgtcga	gcgtgcacgc	gagttggtcg	agaaaagtga	1320
72	tggattggag	aagacgagag	ccttgccgga	ggagtatgcc	cagaaggcgt	tggatgcaat	1380
74	tcggacgttc	ccggagagtc	cggcacggaa	ggctttggag	cagttgacgg	acaaggtgtt	1440
76	gactaggtca	agataggaat	tcgagctcgg	tacccgggga	tcctctagag	tcgacctgca	1500

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78 ggcattgcaag cttggctgtt ttggcggatg agagaagatt ttcagcctga tacagattaa 1560
80 atcagaacgc agaagcggtc tgataaaaca gaatttgcct ggcggcagta gcgcggtggt 1620
82 cccacctgac cccatgccga actcagaagt gaa 1653
85 <210> SEQ ID NO: 2
86 <211> LENGTH: 446
87 <212> TYPE: PRT
88 <213> ORGANISM: Saitoella complicata
90 <400> SEQUENCE: 2
92 Ser Glu Gln Ile Asp Asn Met Ala Ser Pro Ala Leu Arg Ile Arg Ser
93 1 5 10 15
96 Ile Ser Ser Arg Ser Ile Ala Ser Leu Arg Ser Val Thr Leu Arg Thr
97 20 25 30
100 Ala Ser Ala Pro Ser Leu Arg Leu Arg Cys Thr Pro Thr Ser Arg Pro
101 35 40 45
104 Ser Ser Ser Trp Ala Ala Ala Val Ser Ser Ala Ser Arg Leu Val Glu
105 50 55 60
108 Pro Asp Pro Asn Gln Pro Leu Ile Asn Pro Leu Asn Leu Val Gly Pro
109 65 70 75 80
112 Glu Met Ser Asn Leu Thr Ser Asn Ile Arg Ser Leu Leu Gly Ser Gly
113 85 90 95
116 His Pro Ser Leu Asp Thr Val Ala Lys Tyr Tyr Val Gln Ser Glu Gly
117 100 105 110
120 Lys His Ile Arg Pro Leu Met Val Leu Leu Met Ala Gln Ala Thr Glu
121 115 120 125
124 Val Ala Pro Lys Val Gln Gly Trp Glu Lys Val Val Glu Val Pro Val
125 130 135 140
128 Asn Glu Gly Leu Ala Pro Pro Glu Val Leu Asn Asp Lys Asn Pro Asp
129 145 150 155 160
132 Met Met Asn Met Arg Ser Gly Pro Leu Thr Lys Asp Gly Glu Ile Glu
133 165 170 175
136 Gly Gln Thr Ser Asn Ile Leu Ala Ser Gln Arg Arg Leu Ala Glu Ile
137 180 185 190
140 Thr Glu Met Ile His Ala Ala Ser Leu Leu His Asp Asp Val Ile Asp
141 195 200 205
144 Ala Ser Glu Thr Arg Arg Asn Ala Pro Ser Gly Asn Gln Ala Phe Gly
145 210 215 220
148 Asn Lys Met Ala Ile Leu Ala Gly Asp Phe Leu Leu Gly Arg Ala Ser
149 225 230 235 240
152 Val Ala Leu Ala Arg Leu Arg Asn Pro Glu Val Ile Glu Leu Leu Ala
153 245 250 255
156 Thr Val Ile Ala Asn Leu Val Glu Gly Phe Met Gln Leu Lys Asn
157 260 265 270
160 Thr Val Asp Asp Ala Ile Glu Ala Thr Ala Thr Gln Glu Thr Phe Asp
161 275 280 285
164 Tyr Tyr Leu Gln Lys Thr Tyr Leu Lys Thr Ala Ser Leu Ile Ala Lys
165 290 295 300
168 Ser Cys Arg Ala Ser Ala Leu Leu Gly Gly Ala Thr Pro Glu Val Ala
169 305 310 315 320
172 Asp Ala Ala Tyr Ala Tyr Gly Arg Asn Leu Gly Leu Ala Phe Gln Ile

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```

173           325           330           335
176 Val Asp Asp Met Leu Asp Tyr Thr Val Ser Ala Thr Asp Leu Gly Lys
177           340           345           350
180 Pro Ala Gly Ala Asp Leu Gln Leu Gly Leu Ala Thr Ala Pro Ala Leu
181           355           360           365
184 Phe Ala Trp Lys His His Ala Glu Leu Gly Pro Met Ile Lys Arg Lys
185           370           375           380
188 Phe Ser Asp Pro Gly Asp Val Glu Arg Ala Arg Glu Leu Val Glu Lys
189 385           390           395           400
192 Ser Asp Gly Leu Glu Lys Thr Arg Ala Leu Ala Glu Glu Tyr Ala Gln
193           405           410           415
196 Lys Ala Leu Asp Ala Ile Arg Thr Phe Pro Glu Ser Pro Ala Arg Lys
197           420           425           430
200 Ala Leu Glu Gln Leu Thr Asp Lys Val Leu Thr Arg Ser Arg
201           435           440           445

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204 <210> SEQ ID NO: 3

205 <211> LENGTH: 24

206 <212> TYPE: DNA

207 <213> ORGANISM: Artificial Sequence

209 <220> FEATURE:

210 <223> OTHER INFORMATION: Primer DPS-1

213 <220> FEATURE:

214 <221> NAME/KEY: misc_feature

215 <222> LOCATION: (10)..(10)

216 <223> OTHER INFORMATION: n stands for g, a, t, or c

218 <220> FEATURE:

219 <221> NAME/KEY: misc_feature

220 <222> LOCATION: (13)..(13)

221 <223> OTHER INFORMATION: n stands for g, a, t, or c

223 <400> SEQUENCE: 3

W--> 224 aaggatcctn ytncaaggayg aygt

24

227 <210> SEQ ID NO: 4

228 <211> LENGTH: 17

229 <212> TYPE: DNA

230 <213> ORGANISM: Artificial Sequence

232 <220> FEATURE:

233 <223> OTHER INFORMATION: Primer DPS-1 1AS

236 <220> FEATURE:

237 <221> NAME/KEY: misc_feature

238 <222> LOCATION: (6)..(6)

239 <223> OTHER INFORMATION: n stands for g, a, t, or c

241 <220> FEATURE:

242 <221> NAME/KEY: misc_feature

243 <222> LOCATION: (15)..(15)

244 <223> OTHER INFORMATION: n stands for g, a, t, or c

246 <400> SEQUENCE: 4

W--> 247 aytgnadra aytcncc

17

250 <210> SEQ ID NO: 5

251 <211> LENGTH: 21

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Input Set : A:\21581-265.seq.V3.ST25.txt

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252 <212> TYPE: DNA
253 <213> ORGANISM: Artificial Sequence
255 <220> FEATURE:
256 <223> OTHER INFORMATION: Primer Sa-1S
258 <400> SEQUENCE: 5
259 gagaccagac gaaacgcacc a 21
262 <210> SEQ ID NO: 6
263 <211> LENGTH: 21
264 <212> TYPE: DNA
265 <213> ORGANISM: Artificial Sequence
267 <220> FEATURE:
268 <223> OTHER INFORMATION: Primer Sa-2AS
270 <400> SEQUENCE: 6
271 tgggtgcgttt cgtctggtct c 21
274 <210> SEQ ID NO: 7
275 <211> LENGTH: 26
276 <212> TYPE: DNA
277 <213> ORGANISM: Artificial Sequence
279 <220> FEATURE:
280 <223> OTHER INFORMATION: Primer Sa-N1
282 <400> SEQUENCE: 7
283 aacatatggc ctcaccagca ctgcgg 26
286 <210> SEQ ID NO: 8
287 <211> LENGTH: 29
288 <212> TYPE: DNA
289 <213> ORGANISM: Artificial Sequence
291 <220> FEATURE:
292 <223> OTHER INFORMATION: Primer Sa-C
294 <400> SEQUENCE: 8
295 aagaattcct atcttgacct agtcaacac 29
298 <210> SEQ ID NO: 9
299 <211> LENGTH: 8
300 <212> TYPE: PRT
301 <213> ORGANISM: Saitoella complicata
303 <400> SEQUENCE: 9
305 Gly Asp Phe Leu Leu Gly Arg Ala
306 1 5

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RAW SEQUENCE LISTING ERROR SUMMARY
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Input Set : A:\21581-265.seq.V3.ST25.txt
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; N Pos. 10,13

Seq#:4; N Pos. 6,15